FIG. 1

```
  1  CTCTAGATGTACATGGAGGATGACCGAAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA   60
  1                  M  T  E  K  T  N  G  V  K  S  S  P  A  N      14

 61  TAATCACAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC  120
 15   N  H  N  H  H  A  P  P  A  I  K  A  N  G  K  D  D  H  R  T    34

121  AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC  180
 35   S  S  R  P  H  S  A  A  D  D  D  T  S  S  E  L  Q  R  L  A    54

181  AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCCGCAGGATAGTTCGCCTGGTGGG  240
 55   D  V  D  A  P  Q  Q  G  R  S  G  F  R  R  I  V  R  L  V  G    74

241  GATCATCAGAGAATGGGCCAACAAGAATTTCCGAGAGGAGGAACCTAGGCCTGACTCATT  300
 75   I  I  R  E  W  A  N  K  N  F  R  E  E  E  P  R  P  D  S  F    94

301  CCTCGAGCGTTTTCGTGGGCCTGAACTCCAGACTGTGACCACACAGGAGGGGGATGGCAA  360
 95   L  E  R  F  R  G  P  E  L  Q  T  V  T  T  Q  E  G  D  G  K   114

361  AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGGA  420
115   G  D  K  D  G  E  D  K  G  T  K  K  K  F  E  L  F  V  L  D   134

421  CCCAGCTGGGGATTTGTACTACTGCTGGCTATTTGTCATTGCCATGCCCGTCCTTTACAA  480
135   P  A  G  D  L  Y  Y  C  W  L  F  V  I  A  M  P  V  L  Y  N   154

481  CTGGTGCCTGCTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT  540
155   W  C  L  L  V  A  R  A  C  F  S  D  L  Q  K  G  Y  Y  L  V   174

541  GTGGCTGGTGCTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCCGATT  600
175   W  L  V  L  D  Y  V  S  D  V  V  Y  I  A  D  L  F  I  R  L   194

601  GCGCACAGGTTTCCTGGAGCAGGGGCTGCTGGTCAAAGATACCAAGAAACTGCGAGACAA  660
195   R  T  G  F  L  E  Q  G  L  L  V  K  D  T  K  K  L  R  D  N   214

661  CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT  720
215   Y  I  H  T  L  Q  F  K  L  D  V  A  S  I  I  P  T  D  L  I   234

721  CTATTTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCCTGCTGCACTTTGC  780
235   Y  F  A  V  D  I  H  S  P  E  V  R  F  N  R  L  L  H  F  A   254

781  CCGCATGTTTGAGTTCTTTGACCGGACAGAGACACGCACCAACTACCCTAACATCTTCCG  840
255   R  M  F  E  F  F  D  R  T  E  T  R  T  N  Y  P  N  I  F  R   274

841  CATCAGCAACCTTGTCCTCTACATCTTGGTCATCATCCACTGGAATGCCTGCATCTATTA  900
275   I  S  N  L  V  L  Y  I  L  V  I  I  H  W  N  A  C  I  Y  Y   294

901  TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCACTGA  960
295   A  I  S  K  S  I  G  F  G  V  D  T  W  V  Y  P  N  I  T  D   314
```

FIG. 1 (Cont'd)

```
 961  CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC  1020
 315   P  E  Y  G  Y  L  A  R  E  Y  I  Y  C  L  Y  W  S  T  L  T   334


1021  TCTCACTACCATTGGGGAGACACCACCCCCTGTAAAGGATGAGGAGTACCTATTTGTCAT  1080
 335   L  T  T  I  G  E  T  P  P  P  V  K  D  E  E  Y  L  F  V  I   354


1081  CTTTGACTTCCTGATTGGCGTCCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT  1140
 355   F  D  F  L  I  G  V  L  I  F  A  T  I  V  G  N  V  G  S  M   374


1141  GATCTCCAACATGAATGCCACCCGGGCAGAGTTCCAGGCTAAGATCGATGCCGTGAAACA  1200
 375   I  S  N  M  N  A  T  R  A  E  F  Q  A  K  I  D  A  V  K  H   394


1201  CTACATGCAGTTCCGAAAGGTCAGCAAGGGGATGGAAGCCAAGGTCATTAGGTGGTTTGA  1260
 395   Y  M  Q  F  R  K  V  S  K  G  M  E  A  K  V  I  R  W  F  D   414


1261  CTACTTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC  1320
 415   Y  L  W  T  N  K  K  T  V  D  E  R  E  I  L  K  N  L  P  A   434


1321  CAAGCTCAGGGCTGAGATAGCCACCAATGTCCACTTGTCCACACTCAAGAAAGTGCGCAT  1380
 435   K  L  R  A  E  I  A  T  N  V  H  L  S  T  L  K  K  V  R  I   454


1381  CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCTCAGGT  1440
 455   F  H  D  C  E  A  G  L  L  V  E  L  V  L  K  L  R  P  Q  V   474


1441  CTTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT  1500
 475   F  S  P  G  D  Y  I  C  R  K  G  D  I  G  K  E  M  Y  I  I   494


1501  TAAGGAGGGCAAACTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC  1560
 495   K  E  G  K  L  A  V  V  A  D  D  G  V  T  Q  Y  A  L  L  S   514


1561  GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAATGGGCAA  1620
 515   A  G  S  C  F  G  E  I  S  I  L  N  I  K  G  S  K  M  G  N   534


1621  TCGACGCACAGCTAATATCCGCAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCCAAGGA  1680
 535   R  R  T  A  N  I  R  S  L  G  Y  S  D  L  F  C  L  S  K  D   554


1681  TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCCTAGAAGAGAGGGG  1740
 555   D  L  M  E  A  V  T  E  Y  P  D  A  K  K  V  L  E  E  R  G   574


1741  TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAGTGGCAACCAGCATGGA  1800
 575   R  E  I  L  M  K  E  G  L  L  D  E  N  E  V  A  T  S  M  E   594


1801  GGTCGACGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAAACCTTGTACACTCG  1860
 595   V  D  V  Q  E  K  L  G  Q  L  E  T  N  M  E  T  L  Y  T  R   614


1861  CTTTGGCCGCCTGCTGGCTGAGTACACGGGGGGCCCAGCAGAAGCTCAAGCAGCGCATCAC  1920
 615   F  G  R  L  L  A  E  Y  T  G  A  Q  Q  K  L  K  Q  R  I  T   634
```

FIG. 1 (Cont'd)

```
1921  AGTTCTGGAAACCAAGATGAAACAGAACAATGAAGATGACTACCTGTCTGATGGGATGAA  1980
 635   V  L  E  T  K  M  K  Q  N  N  E  D  D  Y  L  S  D  G  M  N   654


1981  CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG  2040
 655   S  P  E  L  A  A  A  D  E  P                                 664


2041  CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTTAGATCTCCGGATTTACAT  2100


2101  GCATTACCCTCATGTTCCCTGAATTCTCCCAAAAGTCTCTCTGACCCTGNGTTTTTGGCC  2160


2161  TAAACATCCAAGATTCCGCCTCGGAT  2186
```

FIG. 2

MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDAPQQGRSGFRRI

VRLVGIIREWANKNFREEEPRPDSFLERFRGPELQTVTTQEGDGKGDKDGEDKGTKKKFELFVLDPAGD

LYYCWLFVIAMPVLYNWCLLVARACFSDLQKGYYLVWLVLDYVSDVVYIADLFIRLRTGFLEQGLLVKD

TKKLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS

NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPV

KDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKGMEAKVIRWFD

YLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLKKVRIFHDCEAGLLVELVLKLRPQVFSPGDYICR

KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLS

KDDLMEAVTEYPDAKKVLEERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLLAE

YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAAADEP

FIG. 3

MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDAPQQGRSGFRRI

VRLVGIIREWANKNFREEEPRPDSFLERFRGPELQTVTTQEGDGKGDKDGEDKGTKKKFELFVLDPAGD

LYY**CWLFVIAMPVLYNWCLLVA**RACFSDLQKGYYL**VWLVLDYVSDVVYIADLFI**RLRTGFLEQGLLVKD

TKKLRDNYI**HTLQFKLDVASIIPTDLIYF**AVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFR**IS**

NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPV

KDEE**YLFVIFDFLIGVLIFATIVG**<u>NVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKGMEAKVIRWFD

YLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLKKVR</u>**IFHDCEAGLLVELVLKLRPQV**FSPGDYICR

KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLS

KDDLMEAVTEYPDAKKVLEERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLLAE

YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAAADEP

FIG. 4

```
                 1                                                50
HBMYCNG     (1)  --------------------------------------------------
CNG2_BOS    (1)  --------------------------------------------------
CNG2_MOUSE  (1)  --------------------------------------------------
CNG2_RAT    (1)  --------------------------------------------------
rACNG       (1)  MSSWRSCARAPLSGSAWRRSAATRRSRRCLKTKRKRWSSGKGTPMQSTQC

                 51                                               100
HBMYCNG     (1)  -----------------MTEKNGVKSSPANNHNHHAPPAIKANGKDDH
CNG2_BOS    (1)  -----------------MTEKANGVKSSPANNHNHHAPPAIKASGKDDH
CNG2_MOUSE  (1)  ----------------MMTEKSNGVKSSPANNHNHHPPPSIKANGKDDH
CNG2_RAT    (1)  ----------------MMTEKSNGVKSSPANNHNHHPPPSIKANGKDDH
rACNG      (51)  ETRRRAQTPCESTGHTWRMTEKSNGVKSSPANNHNHVPAIKANGKDES

                 101                                              150
HBMYCNG    (33)  RTSSRPH-SAADDDTSSELQRLADYDAPQQGRSGFRRIVRLVGTIREWAN
CNG2_BOS   (33)  RASSRPQ-SAAADDTSSELQCLAEMDAPQQRRGGFRRIARLVGVIRELWAY
CNG2_MOUSE (34)  RAGSRPQSVAADDDTSSELQRLAEMDTPRRGRGGFRRIVRLVGTIRDWAN
CNG2_RAT   (34)  RAGSRPQSVAADDDTSDELQRLAEMDTPRRGRGGFQRIVRLVGVIRDWAN
rACNG     (101)  RTRSRPQ-SAADDDTSSELQRLAEMDAPQQRRGGFRRIVRLVGVIRQWAN

                 151                                              200
HBMYCNG    (82)  KNFREEEPRPDSFLERFRGPELQTVTTQSGDGKGDKDGFDKGTKKKFELF
CNG2_BOS   (82)  RNFREEEPRPDSFLERFRGPELQTVTTQQGDGKGDKDGEGKGTKKKFELF
CNG2_MOUSE (84)  KNFREEEPRPDSFLERFRGPELQTVTPHQGDGKGDKDGEGKGTKKKFELF
CNG2_RAT   (84)  KNFREEEPRPDSFLERFRGPELQTVTTQGDGKGCKDGEGKGTKKKFELF
rACNG     (150)  RNFREEEARPDSFLERFRGPELQTVTTQQGDGKGDKDGDGKGTKKKFELF

                 201                                              250
HBMYCNG   (132)  VLDPAGDLYYCWLFVIAMPVLYNWCLLVARACFSDLQKGYFVWLVLDYV
CNG2_BOS  (132)  VLDPAGDWYRWLFIAPVLYNWCLLVARACFSDLQKGYFVWLVLDYV
CNG2_MOUSE(134)  VLDPAGDWYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVWLVLDYF
CNG2_RAT  (134)  VLDPAGDWYRWLFVIAMPVLYNWCLLVARACFSDLQRNYFVWLVLDYF
rACNG     (200)  VLDPAGDWYRWLFVIAMPVLYNWCLLVARACFSDLQRGYFVWLVLDYF

                 251                                              300
HBMYCNG   (182)  SDVVYIADLFIRLRTGFLEQGLLVKDSKKLRDNYIHTLQFKLDVASIIPT
CNG2_BOS  (182)  SDVVYIADLFIRLRTGFLEQGLLVKDSKKLRDNYIHTSQFKLDVASIIPT
CNG2_MOUSE(184)  SDVVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPT
CNG2_RAT  (184)  SDVVYIADLIIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPT
rACNG     (250)  SDVVYIADLFIRLRTGFLEQGLLVKDPKKLRDNYIHTLQFKLDVASIIPT

                 301                                              350
HBMYCNG   (232)  DLIYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRISNLVLY
CNG2_BOS  (232)  DLIYFAVGIHNPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNILLY
CNG2_MOUSE(234)  DLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLY
CNG2_RAT  (234)  DLIYFAVGIHSPEVRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLY
rACNG     (300)  DLIYFAVGIHNPELRFNRLLHFARMFEFFDRTETRTSYPNIFRISNLVLY

                 351                                              400
HBMYCNG   (282)  ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS
CNG2_BOS  (282)  ILIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLSREYIYCLYWS
CNG2_MOUSE(284)  ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS
CNG2_RAT  (284)  ILVIIHWNACIYYVISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS
rACNG     (350)  ILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWS
```

FIG. 4 (Continued)

```
                 401                                              450
HBMYCNG    (332)  TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNAT
CNG2_BOS   (332)  TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNAT
CNG2_MOUSE (334)  TLTLTTIGETPPPVKDEEYLFFIFDFLIGVLIFATIVGNVGSMISNMNAT
CNG2_RAT   (334)  TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNAT
rACNG      (400)  TLTLTTIGETPPPVKDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNAT

                 451                                              500
HBMYCNG    (382)  RAEFQAKIDAVKHYMQFRKVSKEMEAKVIRWFDYLWTNKKTVDEREILKN
CNG2_BOS   (382)  RAEFQAKIDAVKHYMQFRKVSKEMEAKVIRWFDYLWTNKKSVDEREVLKN
CNG2_MOUSE (384)  RAEFQAKIDAVKHYMQFRKVSKEMEAKVIKWFDYLWTNKKTVDEREVLKN
CNG2_RAT   (384)  RAEFQAKIDAVKHYMQFRKVSKEMEAKVIKWFDYLWTNKKTVDEREVLKN
rACNG      (450)  RAEFQAKIDAVKHYMQFRKVSKEMEAKVIKWFDYLWTNKKTVDEREVLKN

                 501                                              550
HBMYCNG    (432)  LPAKLRAEIATNVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPGDYI
CNG2_BOS   (432)  LPAKLRAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPGDYI
CNG2_MOUSE (434)  LPAKLRAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPGDYI
CNG2_RAT   (434)  LPAKLRAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPGDYI
rACNG      (500)  LPAKLRAEIAINVHLSTLKKVRIFQDCEAGLLVELVLKLRPQVFSPGDYI

                 551                                              600
HBMYCNG    (482)  CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK
CNG2_BOS   (482)  CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK
CNG2_MOUSE (484)  CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK
CNG2_RAT   (484)  CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK
rACNG      (550)  CRKGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSK

                 601                                              650
HBMYCNG    (532)  MGNRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAKKVLEERGREILMKE
CNG2_BOS   (532)  MGNRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAKRVLEERGREILMKE
CNG2_MOUSE (534)  MGNRRTGTIRSLGYSDLFCLSKDDLMEAVTEYPDAKKVLEERGREILMKE
CNG2_RAT   (534)  MGNRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAKKVLEERGREILMKE
rACNG      (600)  MGNRRTANIRSLGYSDLFCLSKDDLMEAVTEYPDAKKVLEERGREILMKE

                 651                                              700
HBMYCNG    (582)  GLLDENEVAASMEVDVQEKLGQLETNMETLYTRFRRLLAEYTGAQQKLKQ
CNG2_BOS   (582)  GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAQQKLKQ
CNG2_MOUSE (584)  GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAQQKLKQ
CNG2_RAT   (584)  GLLDENEVAASMEVDVQEKLEQLETNMETLYTRFARLLAEYTGAQQKLKQ
rACNG      (650)  GLLDENEVAASMEVDVQEKLKQLETNMETLYTRFRRLLAEYTGAQQKLKQ

                 701                              733
HBMYCNG    (632)  RITVLETKMKQNNEDDYLSDGMNSPELAAADEP
CNG2_BOS   (632)  RITVLETKMKQNNEDDSLSDGMNSPEPPAEKP-
CNG2_MOUSE (634)  RITVLETKMKQNHEDDYLSDGNTPEPAVAE--
CNG2_RAT   (634)  RITVLETKMKQNHEDDYLSDGNTPEPTAAE--
rACNG      (700)  RITVLKKMKQNTEDDYLSDGMNSPEPAAAEQP
```

FIG. 5

```
  1  CTCTAGATGTACATGGAGGATGACCGAAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA   60
  1                 M  T  E  K  T  N  G  V  K  S  S  P  A  N    14

 61  TAATCACAACCATCATGCACCTCCTGCCATCAAGGCCAATGGCAAAGATGACCACAGGAC  120
 15   N  H  N  H  H  A  P  P  A  I  K  A  N  G  K  D  D  H  R  T   34

121  AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC  180
 35   S  S  R  P  H  S  A  A  D  D  D  T  S  S  E  L  Q  R  L  A   54

181  AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCCGCAGGATAGTTCGCCTGGTGGG  240
 55   D  V  D  A  P  Q  Q  G  R  S  G  F  R  R  I  V  R  L  V  G   74

241  GATCATCAGAGAATGGGCCAACAAGAATTTCCGAGAGGAGGAACCTAGGCCTGACTCATT  300
 75   I  I  R  E  W  A  N  K  N  F  R  E  E  E  P  R  P  D  S  F   94

301  CCTCGAGCGTTTTCGTGGGCCTGAACTCCAGACTGTGACCACACAGGAGGGGGATGGCAA  360
 95   L  E  R  F  R  G  P  E  L  Q  T  V  T  T  Q  E  G  D  G  K  114

361  AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGGA  420
115   G  D  K  D  G  E  D  K  G  T  K  K  K  F  E  L  F  V  L  D  134

421  CCCAGCTGGGGATTTGTACTACTGCTGGCTATTTGTCATTGCCATGCCCGTCCTTTACAA  480
135   P  A  G  D  L  Y  Y  C  W  L  F  V  I  A  M  P  V  L  Y  N  154

481  CTGGTGCCTGCTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT  540
155   W  C  L  L  V  A  R  A  C  F  S  D  L  Q  K  G  Y  Y  L  V  174

541  GTGGCTGGTGCTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCCGATT  600
175   W  L  V  L  D  Y  V  S  D  V  V  Y  I  A  D  L  F  I  R  L  194

601  GCGCACAGGTTTCCTGGAGCAGGGGCTGCTGGTCAAAGATACCAAGAAACTGCGAGACAA  660
195   R  T  G  F  L  E  Q  G  L  L  V  K  D  T  K  K  L  R  D  N  214

661  CTACATCCACACCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT  720
215   Y  I  H  T  L  Q  F  K  L  D  V  A  S  I  I  P  T  D  L  I  234

721  CTATTTTGCTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCCTGCTGCACTTTGC  780
235   Y  F  A  V  D  I  H  S  P  E  V  R  F  N  R  L  L  H  F  A  254

781  CCGCATGTTTGAGTTCTTTGACCGGACAGAGACACGCACCAACTACCCTAACATCTTCCG  840
255   R  M  F  E  F  F  D  R  T  E  T  R  T  N  Y  P  N  I  F  R  274

841  CATCAGCAACCTTGTCCTCTACATCTTGGTCATCATCCACTGGAATGCCTGCATCTATTA  900
275   I  S  N  L  V  L  Y  I  L  V  I  I  H  W  N  A  C  I  Y  Y  294

901  TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCACTGA  960
295   A  I  S  K  S  I  G  F  G  V  D  T  W  V  Y  P  N  I  T  D  314
```

FIG. 5 (Cont'd)

```
 961  CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC  1020
 315    P   E   Y   G   Y   L   A   R   E   Y   I   Y   C   L   Y   W   S   T   L   T   334

1021  TCTCACTACCATTGGGGAGACACCACCCCCTGTAAAGGATGAGGAGTACCTATTTGTCAT  1080
 335    L   T   T   I   G   E   T   P   P   P   V   K   D   E   E   Y   L   F   V   I   354

1081  CTTTGACTTCCTGATTGGCGTCCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT  1140
 355    F   D   F   L   I   G   V   L   I   F   A   T   I   V   G   N   V   G   S   M   374

1141  GATCTCCAACATGAATGCCACCCGGGCAGAGTTCCAGGCTAAGATCGATGCCGTGAAACA  1200
 375    I   S   N   M   N   A   T   R   A   E   F   Q   A   K   I   D   A   V   K   H   394

1201  CTACATGCAGTTCCGAAAGGTCAGCAAGGGGATGGAAGCCAAGGTCATTAGGTGGTTTGA  1260
 395    Y   M   Q   F   R   K   V   S   K   G   M   E   A   K   V   I   R   W   F   D   414

1261  CTACTTGTGGACCAATAAGAAGACAGTGGATGAGCGAGAAATTCTCAAGAATCTGCCAGC  1320
 415    Y   L   W   T   N   K   K   T   V   D   E   R   E   I   L   K   N   L   P   A   434

1321  CAAGCTCAGGGCTGAGATAGCCATCAATGTCCACTTGTCCACACTCAAGAAAGTGCGCAT  1380
 435    K   L   R   A   E   I   A   I   N   V   H   L   S   T   L   K   K   V   R   I   454

1381  CTTCCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAAACTCCGTCCTCAGGT  1440
 455    F   H   D   C   E   A   G   L   L   V   E   L   V   L   K   L   R   P   Q   V   474

1441  CTTCAGTCCTGGGGATTACATTTGCCGCAAAGGGGACATCGGCAAGGAGATGTACATCAT  1500
 475    F   S   P   G   D   Y   I   C   R   K   G   D   I   G   K   E   M   Y   I   I   494

1501  TAAGGAGGGCAAACTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTCTGCTGTC  1560
 495    K   E   G   K   L   A   V   V   A   D   D   G   V   T   Q   Y   A   L   L   S   514

1561  GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAATGGGCAA  1620
 515    A   G   S   C   F   G   E   I   S   I   L   N   I   K   G   S   K   M   G   N   534

1621  TCGACGCACAGCTAATATCCGCAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCCAAGGA  1680
 535    R   R   T   A   N   I   R   S   L   G   Y   S   D   L   F   C   L   S   K   D   554

1681  TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCCTAGAAGAGAGGGG  1740
 555    D   L   M   E   A   V   T   E   Y   P   D   A   K   K   V   L   E   E   R   G   574

1741  TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAACGAAGTGGCAACCAGCATGGA  1800
 575    R   E   I   L   M   K   E   G   L   L   D   E   N   E   V   A   T   S   M   E   594

1801  GGTCGACGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAAACCTTGTACACTCG  1860
 595    V   D   V   Q   E   K   L   G   Q   L   E   T   N   M   E   T   L   Y   T   R   614

1861  CTTTGGCCGCCTGCTGGCTGAGTACACGGGGGCCCAGCAGAAGCTCAAGCAGCGCATCAC  1920
 615    F   G   R   L   L   A   E   Y   T   G   A   Q   Q   K   L   K   Q   R   I   T   634
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FIG. 5 (Cont'd)

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1921  AGTTCTGGAAACCAAGATGAAACAGAACAATGAAGATGACTACCTGTCTGATGGGATGAA  1980
 635    V   L   E   T   K   M   K   Q   N   N   E   D   D   Y   L   S   D   G   M   N    654


1981  CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCAACTGCCTCTCCAG  2040
 655    S   P   E   L   A   A   A   D   E   P                                          664


2041  CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTTAGATCTCCGGATTTACAT  2100


2101  GCATTACCCTCATGTTCCCTGAATTCTCCCAAAAGCCTCTCTGACCCTGGGTTTTTGGCC  2160


2161  TAAACATCCAAGATTCCGCCTCGGATCCCG  2190
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FIG. 6

MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDAPQQGRSGFRRI
VRLVGIIREWANKNFREEEPRPDSFLERFRGPELQTVTTQEGDGKGDKDGEDKGTKKKFELFVLDPAGD
LYYCWLFVIAMPVLYNWCLLVARACFSDLQKGYYLVWLVLDYVSDVVYIADLFIRLRTGFLEQGLLVKD
TKKLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS
NLVLYILVIIHWNACIYYAISKSIGFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPV
KDEEYLFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRKVSKGMEAKVIRWFD
YLWTNKKTVDEREILKNLPAKLRAEIAINVHLSTLKKVRIFHDCEAGLLVELVLKLRPQVFSPGDYICR
KGDIGKEMYIIKEGKLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLS
KDDLMEAVTEYPDAKKVLEERGREILMKEGLLDENEVATSMEVDVQEKLGQLETNMETLYTRFGRLLAE
YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAAADEP

FIG. 7

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  1 MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MTEKTNGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50

 51 QRLADVDAPQQGRSGFRRIVRLVGIIREWANKNFREEEPRPDSFLERFRG 100
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 51 QRLADVDAPQQGRSGFRRIVRLVGIIREWANKNFREEEPRPDSFLERFRG 100

101 PELQTVTTQEGDGKGDKDGEDKGTKKKFELFVLDPAGDLYYCWLFVIAMP 150
    |||||||||||||||||||||||||||||||||||||||||||||||||||
101 PELQTVTTQEGDGKGDKDGEDKGTKKKFELFVLDPAGDLYYCWLFVIAMP 150

151 VLYNWCLLVARACFSDLQKGYYLVWLVLDYVSDVVYIADLFIRLRTGFLE 200
    |||||||||||||||||||||||||||||||||||||||||||||||||||
151 VLYNWCLLVARACFSDLQKGYYLVWLVLDYVSDVVYIADLFIRLRTGFLE 200

201 QGLLVKDTKKLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRL 250
    |||||||||||||||||||||||||||||||||||||||||||||||||||
201 QGLLVKDTKKLRDNYIHTLQFKLDVASIIPTDLIYFAVDIHSPEVRFNRL 250

251 LHFARMFEFFDRTETRTNYPNIFRISNLVLYILVIIHWNACIYYAISKSI 300
    |||||||||||||||||||||||||||||||||||||||||||||||||||
251 LHFARMFEFFDRTETRTNYPNIFRISNLVLYILVIIHWNACIYYAISKSI 300

301 GFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEY 350
    |||||||||||||||||||||||||||||||||||||||||||||||||||
301 GFGVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPVKDEEY 350

351 LFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRK 400
    |||||||||||||||||||||||||||||||||||||||||||||||||||
351 LFVIFDFLIGVLIFATIVGNVGSMISNMNATRAEFQAKIDAVKHYMQFRK 400

401 VSKGMEAKVIRWFDYLWTNKKTVDEREILKNLPAKLRAEIAINVHLSTLK 450
    ||||||||||||||||||||||||||||||||||||||||| |||||||||
401 VSKGMEAKVIRWFDYLWTNKKTVDEREILKNLPAKLRAEIATNVHLSTLK 450

451 KVRIFHDCEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLA 500
    |||||||||||||||||||||||||||||||||||||||||||||||||||
451 KVRIFHDCEAGLLVELVLKLRPQVFSPGDYICRKGDIGKEMYIIKEGKLA 500

501 VVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFC 550
    |||||||||||||||||||||||||||||||||||||||||||||||||||
501 VVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFC 550

551 LSKDDLMEAVTEYPDAKKVLEERGREILMKEGLLDENEVATSMEVDVQEK 600
    |||||||||||||||||||||||||||||||||||||||||||||||||||
551 LSKDDLMEAVTEYPDAKKVLEERGREILMKEGLLDENEVATSMEVDVQEK 600

601 LGQLETNMETLYTRFGRLLAEYTGAQQKLKQRITVLETKMKQNNEDDYLS 650
    |||||||||||||||||||||||||||||||||||||||||||||||||||
601 LGQLETNMETLYTRFGRLLAEYTGAQQKLKQRITVLETKMKQNNEDDYLS 650

651 DGMNSPELAAADEP* 665
    |||||||||||||||
651 DGMNSPELAAADEP. 664
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